Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims:

Claims 1-11 (cancelled)

12. (withdrawn) A method for evaluating the potential of a chemical entity to associate with:

a) a molecule or molecular complex comprising a binding pocket defined by structure coordinates of JNK3 amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å,

said method comprising the steps of:

(i) employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; and

(ii) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket; and

(iii) outputting said quantified association to a suitable output hardware.

13. (withdrawn) The method according to claim 12, wherein said method evaluates the potential of chemical entity to associate with:

a) a molecular or molecular complex comprising a binding pocket defined by the structural coordinates of JNK3 amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207, according to Figure 1; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

14. (withdrawn) The method according to claims 12 or 13, wherein said method evaluates the potential of a chemical entity to associate with a molecule or molecular complex:

a) defined by the set of structure coordinates for JNK3 amino acids, as set forth in Figure 1; or

b) a homologue of said molecule or molecular complex having a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

15. (cancelled)

16. (currently amended) A method for ~~identifying~~ designing an inhibitor of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule, comprising the step of:

using the atomic coordinates in Figure 1A, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, which describe ~~all or part of~~ a binding pocket of the unphosphorylated JNK3, to design or select said inhibitor, ~~which~~ where said binding pocket comprises the ~~atomic coordinates of~~ amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and

Leu206. ~~according to Figure 1A, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to design or select said inhibitor.~~

17. (currently amended) The method according to claim 16, wherein said binding pocket additionally comprises the ~~atomic coordinates of~~ amino acids Ile77, Cys79, Ala80, Val90, Ile92, Lys94, Leu95, His104, Arg107, Ser125, Leu144, Val145, Leu153, Cys154, Asp189, Pro192, Ile195, Val197, Lys204 and Asp207. ~~according to Figure 1A, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.~~

18. (cancelled)

19. (previously presented) The method according to claims 16 or 17, wherein the inhibitor is contacted with said unphosphorylated JNK3 molecule to determine the ability of said inhibitor to interact with the unphosphorylated JNK3 molecule.

20. (currently amended) A method for ~~identifying~~ designing an inhibitor of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule comprising the steps of:

a) producing a crystal of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule and a chemical entity, wherein said unphosphorylated JNK3 molecule contains an N-terminal deletion of 39 amino acids;

b) determining the three-dimensional atomic coordinates of amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 of a binding pocket of the unphosphorylated JNK3 molecule by X-ray diffraction of the crystal;

c) using ~~all or part of~~ said coordinates, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to design or select said inhibitor.

21. (previously presented) The method according to claim 20, further comprising the step of contacting said inhibitor with said unphosphorylated JNK3 molecule to determine the ability of said inhibitor to interact with said unphosphorylated JNK3 molecule.

22. (previously presented) The method according to claim 20, wherein said unphosphorylated JNK3 molecule further contains a C-terminal deletion of 20 amino acids.

23. (new) A method for identifying an inhibitor of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule, comprising the step of:

a) using the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of molecule comprising a JNK3 binding pocket;

b) employing said three-dimensional structure to design or select said potential agonist or antagonist;

c) synthesizing said agonist or antagonist; and

d) contacting said agonist or antagonist with said molecule to determine the ability of said potential agonist or antagonist to interact with said molecule.

24. (new) The method according to claim 23, wherein the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, are used to generate said three-dimensional structure of the molecule comprising a JNK3 binding pocket.

25. (new) A method for identifying an inhibitor of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule, comprising the steps of:

a) producing a crystal of an unphosphorylated JNK3 (c-Jun N-terminal kinase 3) molecule and a chemical entity, wherein said unphosphorylated JNK3 molecule contains an N-terminal deletion of 39 amino acids;

b) determining the three-dimensional atomic coordinates of amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155,

Lys191, Ser193, Asn194, Val196 and Leu206 of a binding pocket of the unphosphorylated JNK3 molecule by X-ray diffraction of the crystal;

c) using the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of molecule comprising a JNK3 binding pocket;

d) employing said three-dimensional structure to design or select said potential agonist or antagonist;

e) synthesizing said agonist or antagonist; and

f) contacting said agonist or antagonist with said molecule to determine the ability of said potential agonist or antagonist to interact with said molecule.

26. (new) The method according to claim 25, wherein the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150,

Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, are used to generate said three-dimensional structure of the molecule comprising a JNK3 binding pocket.